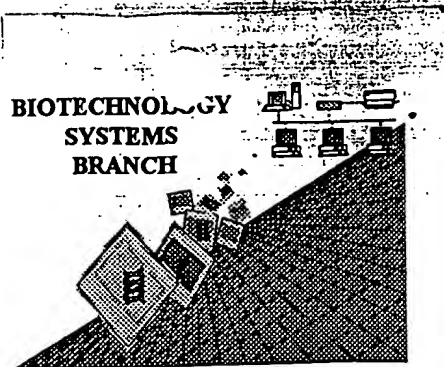


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/524,531

Source: 1646

Date Processed by STIC: 7/28/2000

THE ATTACHED PRINTOUT CONTAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY
EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

R. Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/524,531

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RECEIVED

AUG 08 2000

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/524,531
DATE: 07/28/2000
TIME: 13:29:08

Input Set : A:\imhof.app.txt
Output Set: N:\CRF3\07282000\I524531.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: RMF Dictagene S.A.
5 <120> TITLE OF INVENTION: Vascular adhesion molecules and modulation of their
6 function
8 <130> FILE REFERENCE: rmf6usseqlist
10 <140> CURRENT APPLICATION NUMBER: 09/524531
11 <141> CURRENT FILING DATE: 2000-03-13
13 <150> PRIOR APPLICATION NUMBER: EP 99.200746.8
14 <151> PRIOR FILING DATE: 1999-03-11
16 <160> NUMBER OF SEQ ID NOS: 21
18 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

550 <210> SEQ ID NO: 21
551 <211> LENGTH: 300
552 <212> TYPE: PRT
553 <213> ORGANISM: Mus musculus
555 <400> SEQUENCE: 21
556 Met Gly Thr Glu Gly Lys Ala Gly Arg Lys Leu Leu Phe Leu Phe Thr
557 1 5 10 15
559 Ser Met Ile Leu Gly Ser Leu Val Gln Gly Lys Gly Ser Val Tyr Thr
560 20 25 30
562 Ala Gln Ser Asp Val Gln Val Pro Glu Met Glu Ser Ile Lys Leu Thr
563 35 40 45
565 Cys Thr Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Val
566 50 55 60
568 Gln Gly Ser Thr Thr Ala Leu Val Cys Tyr Asn Ser Gln Ile Thr Ala
569 65 70 75 80
571 Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Glu Gly Ile Thr Phe Ser
572 85 90 95
574 Ser Val Thr Arg Lys Asp Asn Gly Glu Tyr Thr Cys Met Val Ser Glu
575 100 105 110
577 Glu Gly Gly Gln Asn Tyr Gly Glu Val Ser Ile His Leu Thr Val Leu
578 115 120 125
580 Val Pro Pro Ser Lys Pro Thr Ile Ser Val Pro Ser Val Thr Ile
581 130 135 140
583 Gly Asn Arg Ala Val Leu Thr Cys Ser Glu His Asp Gly Ser Pro Pro
584 145 150 155 160
586 Ser Glu Tyr Ser Trp Phe Lys Asp Gly Ile Ser Met Leu Thr Ala Asp
587 165 170 175
589 Ala Lys Lys Thr Arg Ala Phe His Asn Ser Ser Phe Thr Ile Asp Pro
590 180 185 190
592 Lys Ser Gly Asp Leu Tyr Phe Asp Phe Val Thr Ala Phe Asp Ser Gly
593 195 200 205
595 Glu Tyr Tyr Cys Gln Ala Gln Asn Gly Tyr Gly Thr Ala Met Arg Ser
596 210 215 220

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/524,531

DATE: 07/28/2000

TIME: 13:29:08

Input Set : A:\imhof.app.txt

Output Set: N:\CRF3\07282000\I524531.raw

AUG 08 2000

598 Glu Ala Ala His Met Asp Ala Val Glu Leu Asn Val Gly Gly Ile Val
 599 225 230 235 240
 601 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Leu Leu Ile Phe Gly
 602 245 250 255
 604 Val Trp Phe Ala Tyr Ser Arg Gly Tyr Phe Glu Thr Thr Lys Lys Gly
 605 260 265 270
 607 Thr Ala Pro Gly Lys Lys Val Ile Tyr Ser Gln Pro Ser Thr Arg Ser
 608 275 280 285
 610 Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 611 290 295 300
 E--> 615 ??

*delete**see following pages for more error*

RAW SEQUENCE LISTING DATE: 08/04/2000
 PATENT APPLICATION: US/09/524,531 TIME: 15:08:32

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\08042000\I524531.raw

3 <110> APPLICANT: RHF Dictagene S.A.
 5 <120> TITLE OF INVENTION: Vascular adhesion molecules and modulation of their
 6 function
 8 <130> FILE REFERENCE: rmf6usseqlist
 10 <140> CURRENT APPLICATION NUMBER: 09/524531
 11 <141> CURRENT FILING DATE: 2000-03-13
 13 <150> PRIOR APPLICATION NUMBER: EP 99.200746.8
 14 <151> PRIOR FILING DATE: 1999-03-11
 16 <160> NUMBER OF SEQ ID NOS: 21
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 20
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 28 <400> SEQUENCE: 1
 W--> 29 *000* tayagttgyn nngcytcyaa *see item 10 on Error summary sheet* 20
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 20
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Artificial Sequence
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 40 <400> SEQUENCE: 2
 W--> 41 taycrgtgyn nngcytcyaa *item 10* 20
 44 <210> SEQ ID NO: 3
 45 <211> LENGTH: 20
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Artificial Sequence
 49 <220> FEATURE:
 50 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 52 <400> SEQUENCE: 3
 W--> 53 taytaytgyn nngcytcyaa *item 10* 20
 56 <210> SEQ ID NO: 4
 57 <211> LENGTH: 18
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 64 <400> SEQUENCE: 4
 65 gaggtacttg catgtgct 18
 68 <210> SEQ ID NO: 5
 69 <211> LENGTH: 19
 70 <212> TYPE: DNA
 71 <213> ORGANISM: Artificial Sequence
 73 <220> FEATURE:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

4

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/524,531

DATE: 07/28/2000

TIME: 13:29:09

Input Set : A:\imhof.app.txt

Output Set: N:\CRF3\07282000\I524531.raw

L:29 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:29 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:29 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:41 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:41 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:41 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:53 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:53 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:53 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:513 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:513 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:513 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:529 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:529 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:529 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
L:545 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:545 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:545 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:615 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:615 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1